



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2020 – 09:31 AM BST

PDB ID : 3QI9
Title : Crystal structure of mouse CD1d-alpha-phosphatidylinositol with mouse Valpha14-Vbeta6 2A3-D NKT TCR
Authors : Clarke, A.J.; Rossjohn, J.
Deposited on : 2011-01-26
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

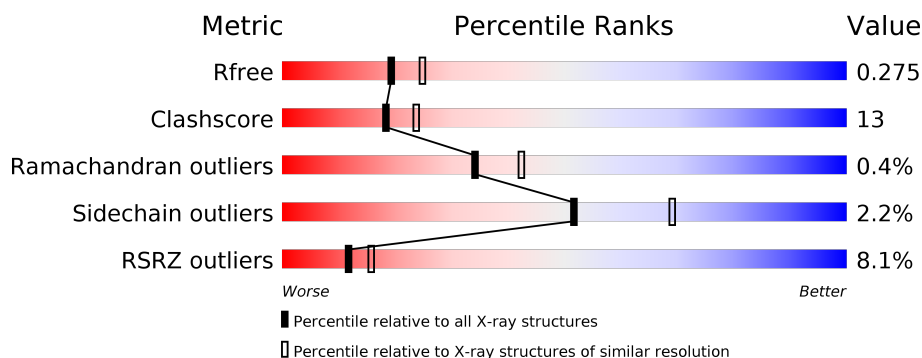
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 80%, yellow 15%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 15% • • </div> </div>
2	B	99	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, green 88%, yellow 12%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 88% 12% </div> </div>
3	C	207	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 16%, green 80%, yellow 13%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 16% 80% 13% • 5% </div> </div>
4	D	243	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 11%, green 83%, yellow 14%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 11% 83% 14% • • </div> </div>
5	E	2	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 100%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% </div> </div>

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6863 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	6	0	0
			2333	1486	406	427	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	conflict	UNP P11609
A	280	GLY	-	expression tag	UNP P11609
A	281	SER	-	expression tag	UNP P11609
A	282	LEU	-	expression tag	UNP P11609
A	283	HIS	-	expression tag	UNP P11609
A	284	HIS	-	expression tag	UNP P11609
A	285	ILE	-	expression tag	UNP P11609
A	286	LEU	-	expression tag	UNP P11609
A	287	ASP	-	expression tag	UNP P11609
A	288	ALA	-	expression tag	UNP P11609
A	289	GLN	-	expression tag	UNP P11609
A	290	LYS	-	expression tag	UNP P11609
A	291	MET	-	expression tag	UNP P11609
A	292	VAL	-	expression tag	UNP P11609
A	293	TRP	-	expression tag	UNP P11609
A	294	ASN	-	expression tag	UNP P11609
A	295	HIS	-	expression tag	UNP P11609
A	296	ARG	-	expression tag	UNP P11609
A	297	HIS	-	expression tag	UNP P11609
A	298	HIS	-	expression tag	UNP P11609
A	299	HIS	-	expression tag	UNP P11609
A	300	HIS	-	expression tag	UNP P11609
A	301	HIS	-	expression tag	UNP P11609
A	302	HIS	-	expression tag	UNP P11609

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	1	0	0
			814	520	138	149	7			

- Molecule 3 is a protein called NKT TCR V alpha 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	196	Total	C	N	O	S	3	0	0
			1514	938	260	309	7			

- Molecule 4 is a protein called NKT TCR V beta 6 2A3-D.

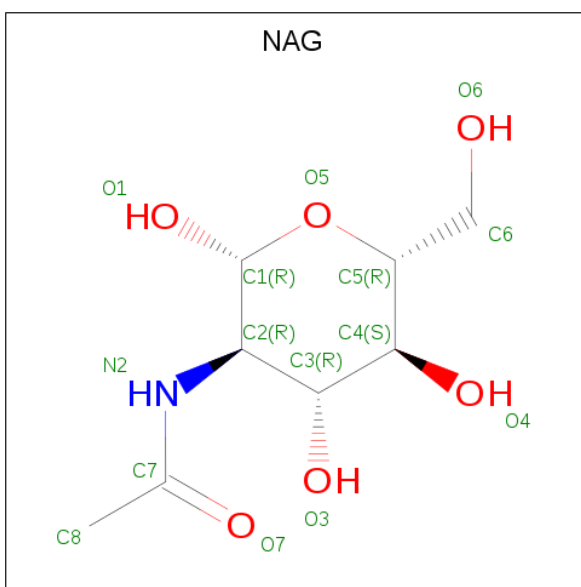
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	239	Total	C	N	O	S	5	0	0
			1897	1201	326	363	7			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



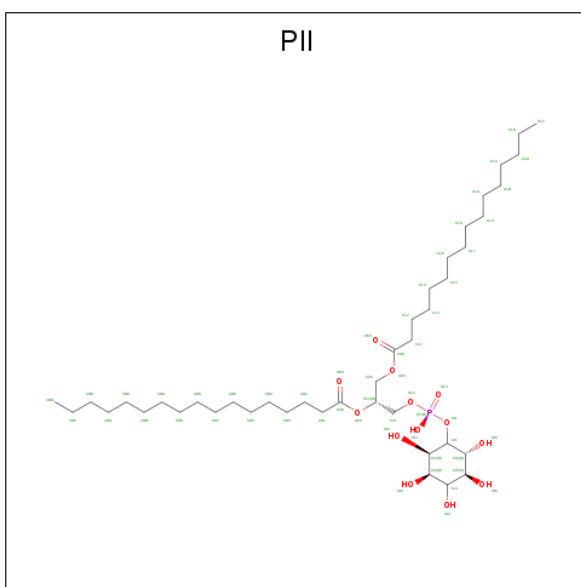
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is 2-[(HYDROXY{(2R,3R,5S,6R)-2,3,4,5,6-PENTAHYDROXYCYCLOHEXYL}OXY)PHOSPHORYL]OXY]-1-[(PALMITOYLOXY)METHYL]ETHYL HEPTADECANOATE (three-letter code: PII) (formula: $C_{42}H_{81}O_{13}P$).

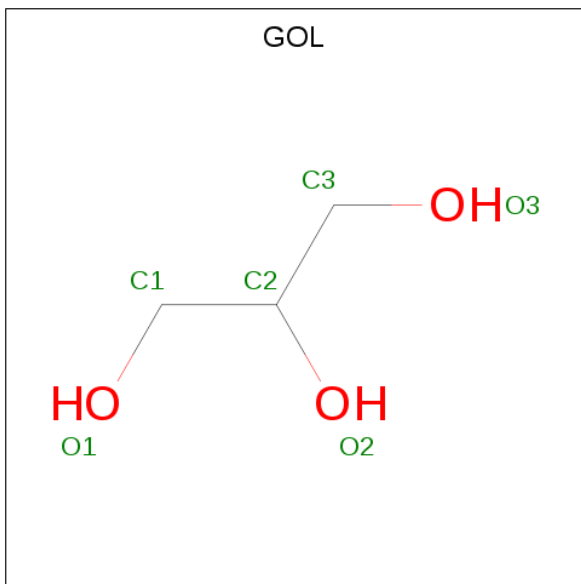


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			56	42	13	1		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Mg	0	0
			1	1		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			6	3	3		
9	D	1	Total	C	O	0	0
			6	3	3		

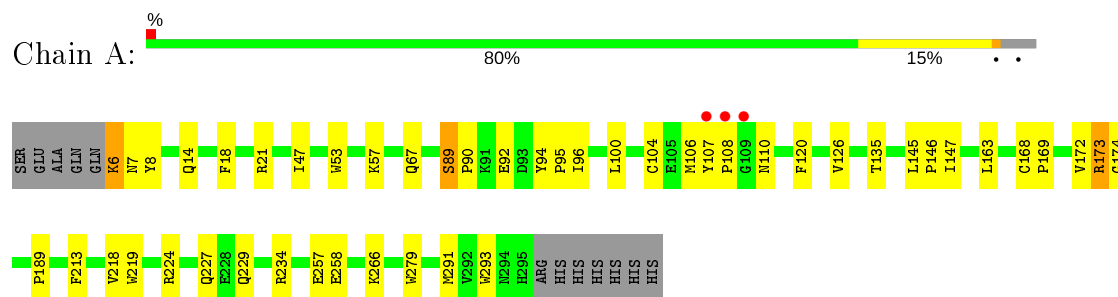
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	68	Total	O	0	0
			68	68		
10	B	26	Total	O	0	0
			26	26		
10	C	38	Total	O	0	0
			38	38		
10	D	48	Total	O	0	0
			48	48		

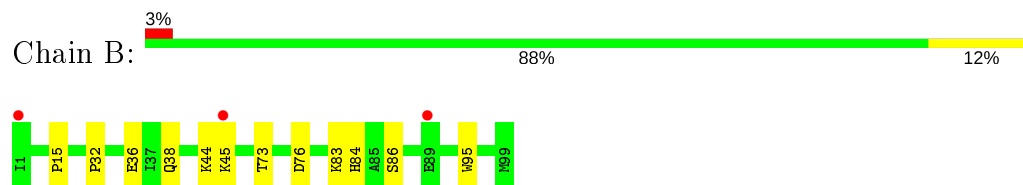
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

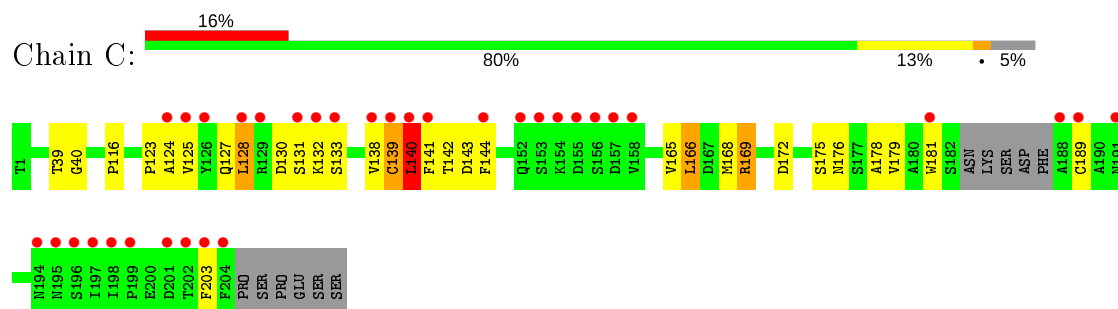
- Molecule 1: Antigen-presenting glycoprotein CD1d1



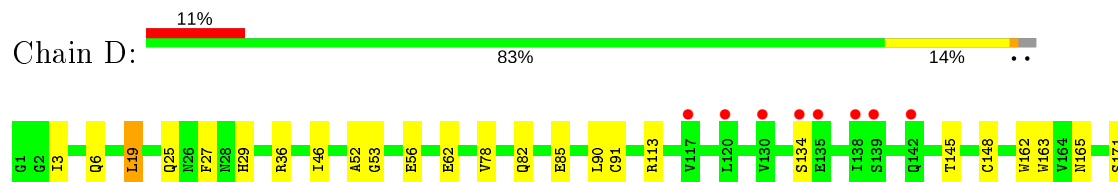
- Molecule 2: Beta-2-microglobulin

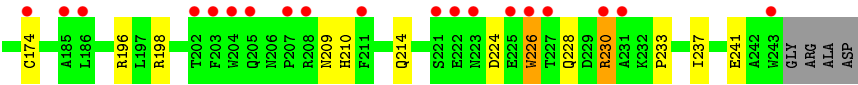


- Molecule 3: NKT TCR V alpha 14



- Molecule 4: NKT TCR V beta 6 2A3-D





- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

100%

NAG1
NAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.70 Å 95.70 Å 289.71 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.31 – 2.30 39.30 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.31-2.30) 100.0 (39.30-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.29 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.247 , 0.275 0.249 , 0.275	Depositor DCC
R_{free} test set	3082 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6863	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, NAG, PII

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.66	2/2403 (0.1%)	0.53	0/3266
2	B	0.50	1/840 (0.1%)	0.50	0/1140
3	C	0.44	0/1539	0.49	0/2089
4	D	0.49	1/1944 (0.1%)	0.51	0/2636
All	All	0.55	4/6726 (0.1%)	0.51	0/9131

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	293	TRP	CD2-CE2	5.18	1.47	1.41
1	A	53	TRP	CD2-CE2	5.16	1.47	1.41
4	D	163	TRP	CD2-CE2	5.08	1.47	1.41
2	B	95	TRP	CD2-CE2	5.04	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2333	0	2232	39	0
2	B	814	0	788	13	1
3	C	1514	0	1466	99	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1897	0	1830	45	0
5	E	28	0	25	0	0
6	A	28	0	26	0	0
7	A	56	0	80	2	0
8	A	1	0	0	0	0
9	B	6	0	8	0	0
9	D	6	0	8	0	0
10	A	68	0	0	1	0
10	B	26	0	0	0	0
10	C	38	0	0	0	0
10	D	48	0	0	0	0
All	All	6863	0	6463	174	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (174) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:141:PHE:CZ	3:C:144:PHE:HB3	1.40	1.56
3:C:168:MET:CE	4:D:198:ARG:HG2	1.31	1.54
3:C:40:GLY:CA	4:D:113:ARG:NH2	1.68	1.52
3:C:141:PHE:CE2	3:C:144:PHE:CD1	2.15	1.32
3:C:168:MET:HE1	4:D:198:ARG:CG	1.59	1.32
3:C:140:LEU:CD1	3:C:179:VAL:CG2	2.08	1.30
3:C:140:LEU:HD13	3:C:179:VAL:CG2	1.63	1.28
3:C:140:LEU:CD1	3:C:179:VAL:HG22	1.60	1.27
3:C:168:MET:CE	4:D:198:ARG:CG	2.13	1.23
3:C:140:LEU:HB2	3:C:178:ALA:O	1.38	1.22
3:C:40:GLY:HA2	4:D:113:ARG:NH2	1.33	1.18
3:C:40:GLY:HA3	4:D:113:ARG:NH2	1.52	1.17
3:C:141:PHE:CZ	3:C:144:PHE:CB	2.29	1.14
2:B:38:GLN:NE2	2:B:45:LYS:HE2	1.60	1.14
1:A:89:SER:HB3	1:A:90:PRO:CD	1.72	1.13
3:C:141:PHE:HZ	3:C:144:PHE:CB	1.61	1.12
3:C:140:LEU:HD12	3:C:179:VAL:HG23	1.32	1.12
1:A:89:SER:HB3	1:A:90:PRO:HD3	1.14	1.10
3:C:168:MET:HE2	4:D:198:ARG:HG2	1.26	1.10
1:A:89:SER:CB	1:A:90:PRO:CD	2.29	1.08
3:C:168:MET:HE1	4:D:198:ARG:HG2	1.14	1.05
3:C:123:PRO:HA	3:C:141:PHE:HE1	1.14	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:145:THR:HG22	4:D:198:ARG:HD2	1.39	1.04
2:B:38:GLN:NE2	2:B:45:LYS:CE	2.21	1.02
3:C:140:LEU:CB	3:C:178:ALA:O	2.08	1.02
3:C:141:PHE:CE2	3:C:144:PHE:CG	2.48	1.00
3:C:140:LEU:CD1	3:C:179:VAL:HG23	1.84	1.00
2:B:38:GLN:HE22	2:B:45:LYS:CE	1.73	0.99
3:C:168:MET:HE1	4:D:198:ARG:HG3	1.45	0.98
3:C:139:CYS:O	3:C:140:LEU:HB3	1.65	0.97
3:C:123:PRO:CA	3:C:141:PHE:HE1	1.78	0.96
3:C:125:VAL:HG12	3:C:141:PHE:HB2	1.47	0.96
3:C:140:LEU:HD12	3:C:179:VAL:CG2	1.89	0.95
3:C:166:LEU:HD22	3:C:166:LEU:O	1.65	0.95
2:B:38:GLN:HE22	2:B:45:LYS:NZ	1.65	0.95
3:C:123:PRO:HA	3:C:141:PHE:CE1	2.04	0.93
1:A:6:LYS:HA	1:A:107:TYR:HD1	1.34	0.90
3:C:141:PHE:CE2	3:C:144:PHE:HB3	2.09	0.87
3:C:140:LEU:CB	3:C:179:VAL:HA	2.07	0.84
3:C:40:GLY:CA	4:D:113:ARG:HH22	1.89	0.84
3:C:141:PHE:CZ	3:C:144:PHE:CD1	2.67	0.82
3:C:125:VAL:CG1	3:C:141:PHE:HB2	2.08	0.82
3:C:166:LEU:HD13	3:C:166:LEU:H	1.44	0.82
3:C:140:LEU:CG	3:C:178:ALA:O	2.28	0.82
3:C:140:LEU:HB2	3:C:179:VAL:HA	1.62	0.82
1:A:6:LYS:HA	1:A:107:TYR:CD1	2.15	0.81
3:C:141:PHE:CE2	3:C:144:PHE:HD1	1.91	0.81
3:C:140:LEU:O	3:C:140:LEU:HD23	1.82	0.80
3:C:40:GLY:HA3	4:D:113:ARG:HH22	1.44	0.80
1:A:89:SER:CB	1:A:90:PRO:HD3	1.96	0.79
2:B:38:GLN:HE22	2:B:45:LYS:HE2	1.31	0.79
3:C:141:PHE:HE2	3:C:144:PHE:CG	1.98	0.78
3:C:125:VAL:HG12	3:C:141:PHE:CB	2.14	0.78
4:D:230:ARG:HG3	4:D:230:ARG:HH21	1.47	0.78
3:C:140:LEU:HD13	3:C:179:VAL:HG22	0.80	0.77
3:C:168:MET:HE3	4:D:198:ARG:HG2	1.64	0.76
1:A:168:CYS:O	1:A:172:VAL:HG23	1.86	0.74
1:A:89:SER:CB	1:A:90:PRO:HD2	2.17	0.74
3:C:40:GLY:N	4:D:113:ARG:NH2	2.34	0.74
3:C:141:PHE:CE2	3:C:144:PHE:CB	2.67	0.73
2:B:38:GLN:NE2	2:B:45:LYS:NZ	2.37	0.73
2:B:38:GLN:CD	2:B:45:LYS:HE2	2.08	0.73
3:C:123:PRO:CA	3:C:141:PHE:CE1	2.67	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:138:VAL:HG13	3:C:138:VAL:O	1.90	0.70
3:C:141:PHE:CZ	3:C:144:PHE:CG	2.79	0.69
1:A:89:SER:HB2	1:A:90:PRO:HD2	1.75	0.67
3:C:169:ARG:HG3	4:D:171:SER:HB3	1.76	0.67
1:A:89:SER:HB2	1:A:90:PRO:CD	2.26	0.66
3:C:166:LEU:HD22	3:C:166:LEU:C	2.17	0.65
1:A:135:THR:HG23	1:A:147:ILE:HD12	1.77	0.65
3:C:141:PHE:CZ	3:C:144:PHE:HD1	2.13	0.64
3:C:141:PHE:HE2	3:C:144:PHE:CD1	2.03	0.64
3:C:166:LEU:H	3:C:166:LEU:CD1	2.11	0.63
3:C:168:MET:HE2	4:D:198:ARG:CG	2.01	0.63
4:D:36:ARG:HB2	4:D:46:ILE:HD11	1.81	0.63
4:D:6:GLN:NE2	4:D:91:CYS:H	1.96	0.63
1:A:168:CYS:HB3	1:A:169:PRO:HD3	1.78	0.63
3:C:166:LEU:HD13	3:C:175:SER:O	1.99	0.63
4:D:25:GLN:HE22	4:D:29:HIS:H	1.47	0.62
4:D:25:GLN:NE2	4:D:29:HIS:H	1.97	0.62
3:C:166:LEU:CD1	3:C:175:SER:O	2.48	0.61
3:C:140:LEU:HB2	3:C:178:ALA:C	2.20	0.61
1:A:219:TRP:HB3	1:A:266:LYS:HB2	1.83	0.60
3:C:141:PHE:CD2	3:C:144:PHE:CD1	2.84	0.60
3:C:140:LEU:HB3	3:C:179:VAL:HA	1.82	0.60
1:A:7:ASN:HB3	1:A:8:TYR:CD2	2.37	0.59
1:A:110:ASN:OD1	1:A:173:ARG:NH1	2.36	0.58
3:C:168:MET:HE2	4:D:198:ARG:CB	2.32	0.58
3:C:124:ALA:N	3:C:141:PHE:CD1	2.72	0.58
3:C:139:CYS:CB	3:C:189:CYS:HG	2.12	0.57
3:C:124:ALA:O	3:C:141:PHE:HA	2.05	0.57
3:C:138:VAL:HG23	3:C:181:TRP:HB3	1.84	0.57
3:C:166:LEU:HB3	4:D:174:CYS:HB2	1.87	0.57
3:C:139:CYS:CB	3:C:189:CYS:SG	2.92	0.56
1:A:189:PRO:HB3	1:A:213:PHE:HB3	1.88	0.56
1:A:145:LEU:HB3	1:A:146:PRO:HD3	1.88	0.56
3:C:140:LEU:O	3:C:140:LEU:CD2	2.54	0.55
3:C:168:MET:HE2	4:D:198:ARG:HB3	1.87	0.55
4:D:230:ARG:NH2	4:D:230:ARG:HG3	2.21	0.55
2:B:32:PRO:O	2:B:84:HIS:HE1	1.90	0.55
3:C:140:LEU:HD12	3:C:178:ALA:O	2.08	0.54
2:B:38:GLN:HE22	2:B:45:LYS:HZ1	1.48	0.54
3:C:124:ALA:N	3:C:141:PHE:CE1	2.76	0.53
1:A:110:ASN:HA	1:A:173:ARG:NH1	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLN:HB3	1:A:100:LEU:HB3	1.90	0.53
3:C:123:PRO:HB3	3:C:141:PHE:CE1	2.43	0.53
4:D:165:ASN:HD21	4:D:209:ASN:HA	1.75	0.52
4:D:6:GLN:HE22	4:D:90:LEU:HA	1.74	0.52
2:B:36:GLU:HB3	2:B:83:LYS:HB3	1.91	0.52
1:A:18:PHE:HB2	1:A:96:ILE:HB	1.92	0.52
4:D:25:GLN:HE21	4:D:27:PHE:N	2.08	0.52
3:C:140:LEU:HG	3:C:178:ALA:O	2.07	0.51
3:C:166:LEU:N	3:C:166:LEU:CD1	2.74	0.51
1:A:94:TYR:HB3	1:A:95:PRO:HA	1.92	0.51
3:C:140:LEU:CD1	3:C:178:ALA:O	2.59	0.51
1:A:21:ARG:NH1	4:D:56:GLU:OE2	2.44	0.50
4:D:145:THR:CG2	4:D:198:ARG:HD2	2.28	0.50
1:A:104:CYS:SG	1:A:172:VAL:HG21	2.51	0.50
3:C:138:VAL:O	3:C:138:VAL:CG1	2.60	0.49
3:C:172:ASP:O	3:C:172:ASP:OD1	2.30	0.49
4:D:19:LEU:HB2	4:D:78:VAL:HB	1.94	0.49
3:C:141:PHE:HZ	3:C:144:PHE:HB3	0.66	0.48
4:D:165:ASN:ND2	4:D:210:HIS:H	2.12	0.47
7:A:405:PII:H212	7:A:405:PII:OC6	2.13	0.47
3:C:123:PRO:CB	3:C:141:PHE:CE1	2.97	0.47
4:D:25:GLN:HE21	4:D:27:PHE:H	1.62	0.47
1:A:126:VAL:HG22	1:A:147:ILE:HD11	1.97	0.47
1:A:258:GLU:HB3	1:A:279:TRP:CD1	2.50	0.47
4:D:224:ASP:OD1	4:D:224:ASP:N	2.48	0.47
1:A:218:VAL:O	1:A:234:ARG:NH2	2.47	0.46
1:A:163:LEU:HD13	7:A:405:PII:HR72	1.98	0.46
3:C:140:LEU:HB2	3:C:179:VAL:CA	2.40	0.46
1:A:227:GLN:HE21	1:A:229:GLN:HE22	1.64	0.46
3:C:125:VAL:HG12	3:C:141:PHE:CA	2.45	0.45
3:C:168:MET:CE	4:D:198:ARG:CB	2.88	0.45
3:C:124:ALA:H	3:C:141:PHE:HD1	1.64	0.45
3:C:165:VAL:HG22	3:C:176:ASN:OD1	2.17	0.45
3:C:116:PRO:HG3	3:C:165:VAL:HG21	1.98	0.45
3:C:125:VAL:HA	3:C:141:PHE:HA	1.99	0.44
4:D:230:ARG:CG	4:D:230:ARG:HH21	2.24	0.44
1:A:47:ILE:H	1:A:67:GLN:HE21	1.66	0.44
1:A:6:LYS:N	1:A:108:PRO:HD2	2.33	0.44
3:C:128:LEU:N	3:C:128:LEU:HD22	2.33	0.44
1:A:174:GLY:HA3	10:A:506:HOH:O	2.17	0.44
3:C:124:ALA:O	3:C:141:PHE:HD1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:145:THR:HG22	4:D:198:ARG:CD	2.29	0.43
3:C:131:SER:HA	3:C:132:LYS:HA	1.70	0.43
3:C:124:ALA:N	3:C:141:PHE:HD1	2.13	0.43
3:C:128:LEU:CD1	4:D:134:SER:HB2	2.48	0.43
3:C:127:GLN:O	3:C:128:LEU:HD13	2.18	0.43
1:A:224:ARG:NH2	1:A:257:GLU:O	2.51	0.43
4:D:214:GLN:HG3	4:D:237:ILE:HG23	2.01	0.43
3:C:140:LEU:HD12	3:C:178:ALA:C	2.38	0.43
1:A:110:ASN:HA	1:A:173:ARG:HH12	1.83	0.43
2:B:84:HIS:HD2	2:B:86:SER:OG	2.01	0.43
1:A:106:MET:CG	1:A:172:VAL:HG11	2.49	0.43
1:A:92:GLU:CG	1:A:120:PHE:HZ	2.32	0.43
1:A:92:GLU:HG2	1:A:120:PHE:CZ	2.54	0.42
4:D:148:CYS:HB2	4:D:162:TRP:CZ2	2.55	0.42
3:C:123:PRO:HB3	3:C:141:PHE:CZ	2.54	0.42
3:C:128:LEU:HD13	4:D:134:SER:HB2	2.01	0.42
4:D:226:TRP:CZ2	4:D:233:PRO:HD3	2.55	0.42
3:C:124:ALA:HB2	3:C:203:PHE:HB3	2.01	0.42
1:A:57:LYS:HD2	1:A:174:GLY:HA2	2.02	0.42
3:C:127:GLN:C	3:C:128:LEU:HD13	2.39	0.42
1:A:92:GLU:HG2	1:A:120:PHE:HZ	1.83	0.42
3:C:141:PHE:CE1	3:C:142:THR:O	2.73	0.42
4:D:52:ALA:HA	4:D:53:GLY:HA2	1.76	0.41
3:C:142:THR:OG1	3:C:143:ASP:N	2.53	0.41
1:A:291:MET:HG2	2:B:15:PRO:HG2	2.03	0.41
4:D:230:ARG:NH2	4:D:230:ARG:CG	2.84	0.41
3:C:125:VAL:HG13	3:C:141:PHE:HB2	2.00	0.41
4:D:82:GLN:HB2	4:D:85:GLU:HB2	2.02	0.41
2:B:73:THR:OG1	2:B:76:ASP:HB2	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:44:LYS:NZ	3:C:133:SER:OG[6_534]	1.89	0.31

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	288/302 (95%)	282 (98%)	5 (2%)	1 (0%)	41	50
2	B	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
3	C	192/207 (93%)	181 (94%)	9 (5%)	2 (1%)	15	17
4	D	237/243 (98%)	229 (97%)	8 (3%)	0	100	100
All	All	814/851 (96%)	787 (97%)	24 (3%)	3 (0%)	34	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	SER
3	C	140	LEU
3	C	130	ASP

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	253/264 (96%)	251 (99%)	2 (1%)	81	91
2	B	92/93 (99%)	92 (100%)	0	100	100
3	C	175/186 (94%)	169 (97%)	6 (3%)	37	51
4	D	206/208 (99%)	198 (96%)	8 (4%)	32	46
All	All	726/751 (97%)	710 (98%)	16 (2%)	52	69

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	173	ARG
3	C	39	THR
3	C	128	LEU
3	C	139	CYS
3	C	140	LEU
3	C	166	LEU
3	C	169	ARG
4	D	3	ILE
4	D	19	LEU
4	D	62	GLU
4	D	196	ARG
4	D	226	TRP
4	D	228	GLN
4	D	230	ARG
4	D	241	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	117	HIS
1	A	154	GLN
1	A	186	GLN
1	A	227	GLN
1	A	230	GLN
2	B	29	GLN
2	B	38	GLN
2	B	84	HIS
3	C	194	ASN
4	D	6	GLN
4	D	25	GLN
4	D	165	ASN
4	D	178	GLN
4	D	187	ASN
4	D	228	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	NAG	E	1	1,5	14,14,15	0.55	0	17,19,21	1.14	2 (11%)
5	NAG	E	2	5	14,14,15	0.63	0	17,19,21	1.10	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	E	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	2	NAG	C4-C3-C2	2.74	115.03	111.02
5	E	1	NAG	O4-C4-C3	-2.61	104.30	110.35
5	E	1	NAG	C4-C3-C2	2.60	114.83	111.02

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	1	NAG	C4-C5-C6-O6

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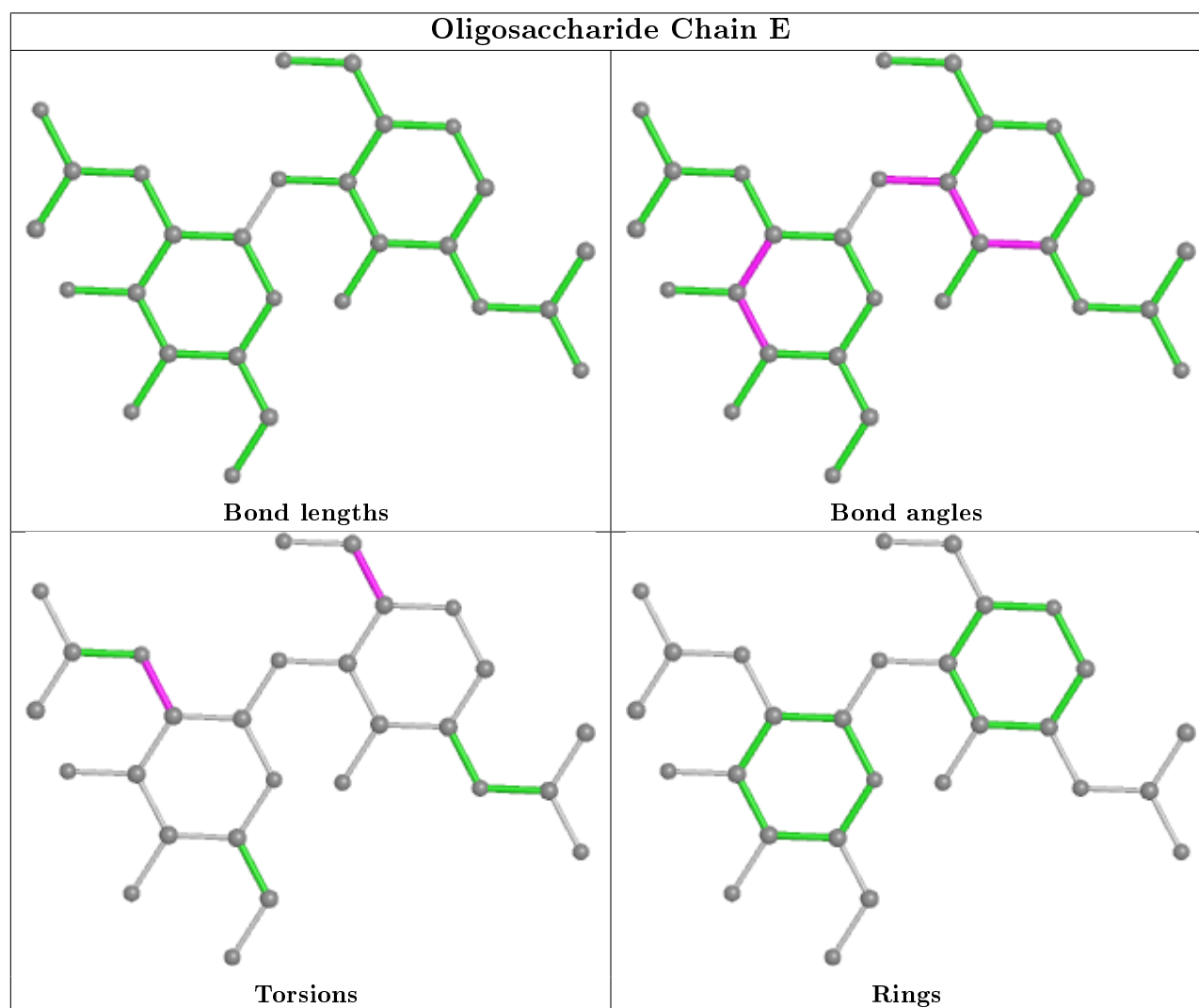
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Mol	Chain	Res	Type	Atoms
5	E	1	NAG	O5-C5-C6-O6
5	E	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	GOL	D	300	-	5,5,5	0.28	0	5,5,5	0.23	0
6	NAG	A	402	1	14,14,15	0.45	0	17,19,21	1.17	1 (5%)
9	GOL	B	100	-	5,5,5	0.27	0	5,5,5	0.34	0
6	NAG	A	401	1	14,14,15	0.43	0	17,19,21	1.68	2 (11%)
7	PII	A	405	-	56,56,56	2.06	3 (5%)	66,68,68	2.46	11 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GOL	D	300	-	-	0/4/4/4	-
6	NAG	A	402	1	-	4/6/23/26	0/1/1/1
9	GOL	B	100	-	-	2/4/4/4	-
6	NAG	A	401	1	-	4/6/23/26	0/1/1/1
7	PII	A	405	-	-	23/51/75/75	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	405	PII	OC9-CO9	12.95	1.61	1.22
7	A	405	PII	C21-C24	-6.04	1.32	1.50
7	A	405	PII	C25-C24	2.89	1.59	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	405	PII	O29-CO9-OC9	-11.50	95.91	123.70
7	A	405	PII	C25-C24-C21	-8.74	91.11	111.79
7	A	405	PII	O29-C24-C21	7.65	136.11	108.40
7	A	405	PII	P1-O12-C21	6.43	159.38	121.68
6	A	401	NAG	C1-O5-C5	4.77	118.66	112.19
7	A	405	PII	O26-C25-C24	4.61	121.86	108.43
7	A	405	PII	O29-CO9-CR1	3.82	119.72	111.50
6	A	402	NAG	C1-O5-C5	3.40	116.79	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	401	NAG	O5-C1-C2	-3.39	105.94	111.29
7	A	405	PII	OC9-CO9-CR1	-3.20	111.25	123.73
7	A	405	PII	P1-OI1-CI1	2.99	130.30	119.41
7	A	405	PII	O26-CO6-CL1	2.28	119.06	111.91
7	A	405	PII	O29-C24-C25	2.25	116.55	108.40
7	A	405	PII	OI1-CI1-CI6	2.24	113.87	108.66

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	100	GOL	O1-C1-C2-C3
7	A	405	PII	CI6-CI1-OI1-P1
7	A	405	PII	OC9-CO9-O29-C24
7	A	405	PII	CR1-CO9-O29-C24
6	A	401	NAG	C8-C7-N2-C2
6	A	401	NAG	O7-C7-N2-C2
6	A	401	NAG	C4-C5-C6-O6
6	A	402	NAG	C8-C7-N2-C2
6	A	402	NAG	O7-C7-N2-C2
6	A	401	NAG	O5-C5-C6-O6
6	A	402	NAG	O5-C5-C6-O6
7	A	405	PII	CRC-CRD-CRE-CRF
7	A	405	PII	CL8-CL9-CLA-CLB
7	A	405	PII	C25-C24-O29-CO9
7	A	405	PII	CLA-CLB-CLC-CLD
7	A	405	PII	CR9-CRA-CRB-CRC
9	B	100	GOL	O1-C1-C2-O2
7	A	405	PII	CR7-CR8-CR9-CRA
7	A	405	PII	CL5-CL6-CL7-CL8
7	A	405	PII	CR6-CR7-CR8-CR9
6	A	402	NAG	C4-C5-C6-O6
7	A	405	PII	CR5-CR6-CR7-CR8
7	A	405	PII	O12-C21-C24-C25
7	A	405	PII	CR4-CR5-CR6-CR7
7	A	405	PII	O12-C21-C24-O29
7	A	405	PII	CR2-CR3-CR4-CR5
7	A	405	PII	CRB-CRC-CRD-CRE
7	A	405	PII	CR1-CR2-CR3-CR4
7	A	405	PII	CL6-CL7-CL8-CL9
7	A	405	PII	C21-C24-C25-O26
7	A	405	PII	CRA-CRB-CRC-CRD

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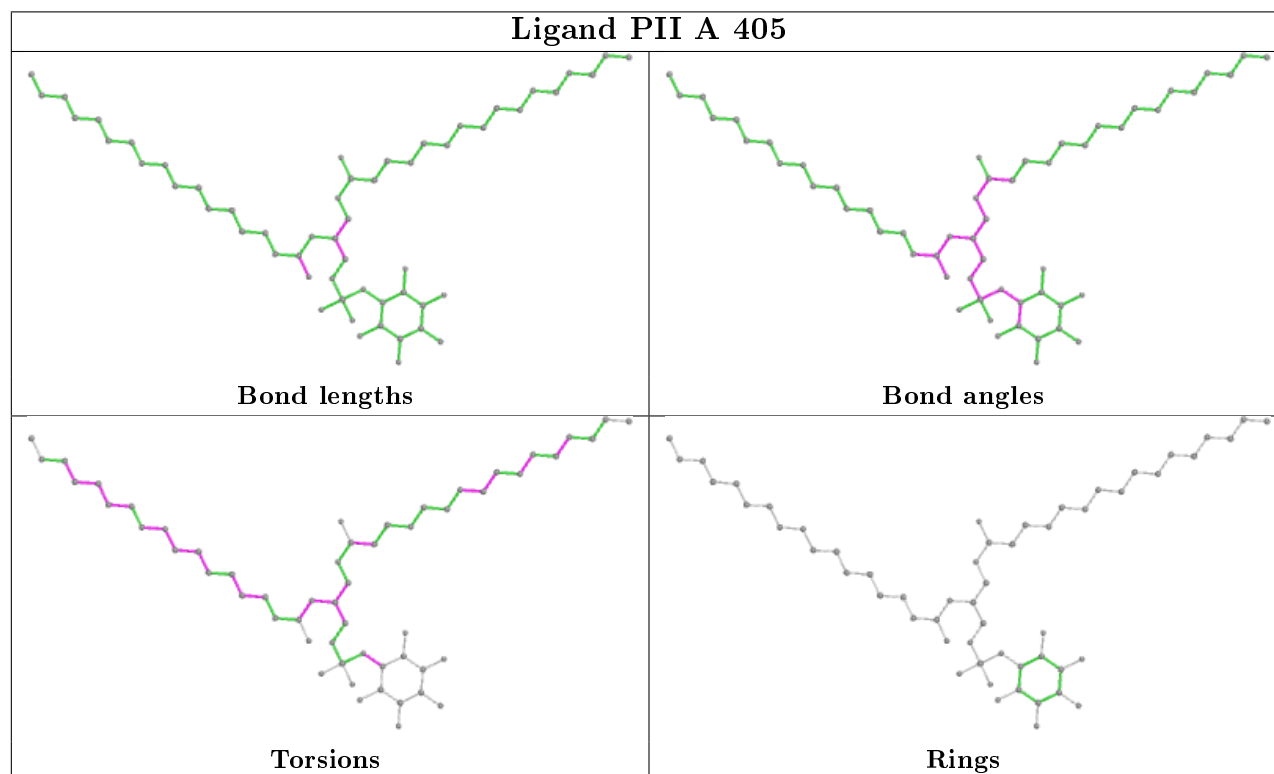
Mol	Chain	Res	Type	Atoms
7	A	405	PII	CL2-CL1-CO6-O26
7	A	405	PII	CL2-CL1-CO6-OC6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	405	PII	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	290/302 (96%)	0.26	3 (1%) 82 86	33, 45, 59, 82	5 (1%)
2	B	99/99 (100%)	0.30	3 (3%) 50 57	34, 46, 61, 73	1 (1%)
3	C	196/207 (94%)	0.91	34 (17%) 1 1	29, 49, 113, 124	2 (1%)
4	D	239/243 (98%)	0.82	27 (11%) 5 7	31, 63, 94, 103	3 (1%)
All	All	824/851 (96%)	0.58	67 (8%) 12 16	29, 48, 96, 124	11 (1%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	141	PHE	9.5
3	C	140	LEU	6.9
3	C	133	SER	6.0
3	C	132	LYS	5.8
4	D	211	PHE	5.3
3	C	154	LYS	5.3
3	C	197	ILE	4.8
3	C	198	ILE	4.6
4	D	204	TRP	4.5
4	D	185	ALA	4.5
3	C	194	ASN	4.5
3	C	188	ALA	4.4
3	C	152	GLN	4.4
3	C	139	CYS	4.2
3	C	196	SER	4.2
4	D	205	GLN	4.2
4	D	138	ILE	4.1
3	C	157	ASP	4.0
4	D	223	ASN	3.7
4	D	227	THR	3.6
3	C	204	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
3	C	155	ASP	3.6
3	C	158	VAL	3.5
4	D	186	LEU	3.5
3	C	181	TRP	3.5
4	D	203	PHE	3.4
4	D	226	TRP	3.4
4	D	134	SER	3.4
3	C	202	THR	3.4
4	D	222	GLU	3.3
4	D	139	SER	3.2
3	C	125	VAL	3.2
3	C	156	SER	3.2
3	C	124	ALA	3.2
3	C	201	ASP	3.2
4	D	243	TRP	3.1
3	C	203	PHE	3.1
3	C	153	SER	3.0
4	D	135	GLU	3.0
4	D	221	SER	3.0
4	D	202	THR	2.8
3	C	129	ARG	2.8
4	D	208	ARG	2.8
1	A	109	GLY	2.7
1	A	108	PRO	2.6
3	C	191	ASN	2.5
4	D	117	VAL	2.5
2	B	45	LYS	2.5
3	C	126	TYR	2.5
4	D	120	LEU	2.5
1	A	107	TYR	2.4
2	B	1	ILE	2.3
2	B	89	GLU	2.3
4	D	174	CYS	2.3
3	C	199	PRO	2.2
4	D	231	ALA	2.2
3	C	138	VAL	2.2
4	D	130	VAL	2.2
4	D	207	PRO	2.2
3	C	128	LEU	2.1
4	D	142	GLN	2.1
4	D	230	ARG	2.1
3	C	131	SER	2.1

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Mol	Chain	Res	Type	RSRZ
4	D	225	GLU	2.1
3	C	189	CYS	2.1
3	C	144	PHE	2.1
3	C	195	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

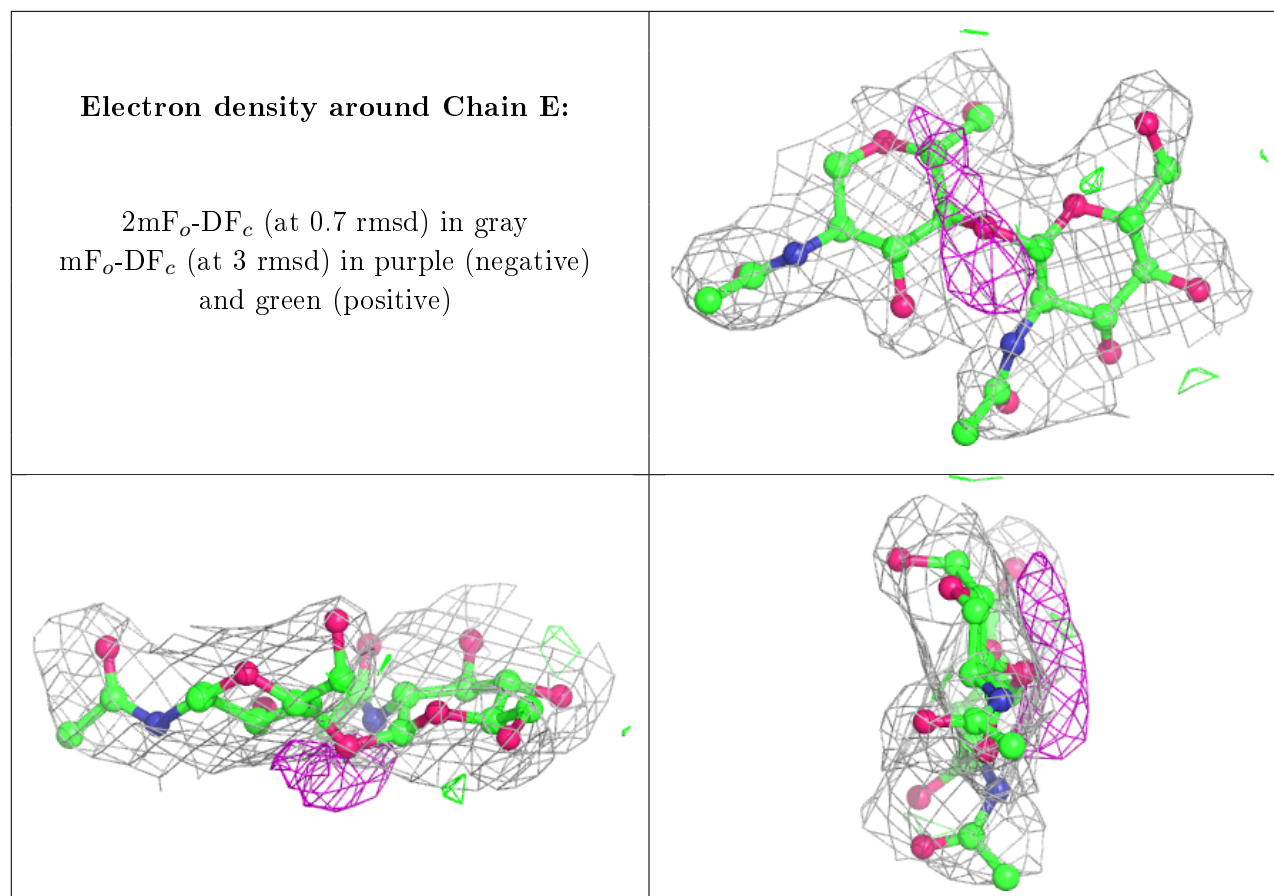
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	E	2	14/15	0.78	0.19	71,74,79,81	0
5	NAG	E	1	14/15	0.91	0.15	56,58,62,67	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands ⓘ

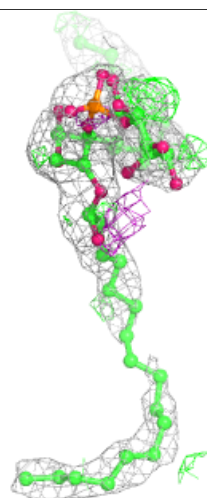
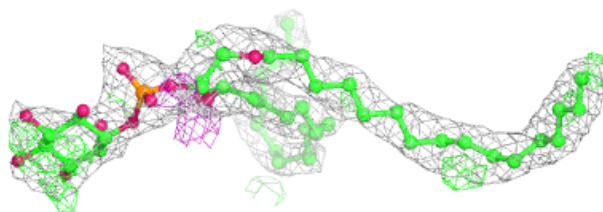
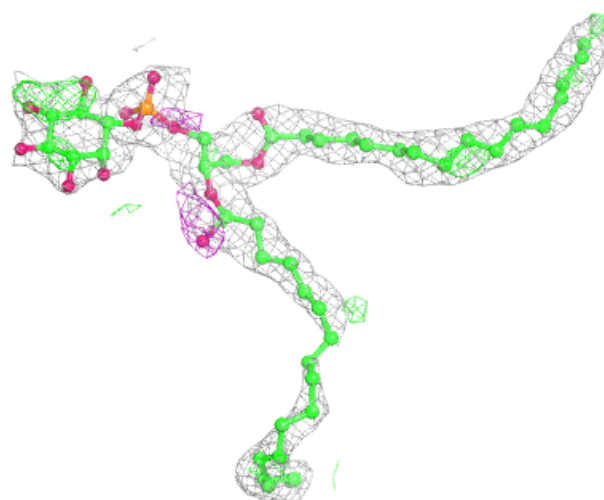
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	GOL	B	100	6/6	0.68	0.22	66,67,69,70	0
6	NAG	A	401	14/15	0.71	0.39	52,54,55,55	0
9	GOL	D	300	6/6	0.74	0.33	70,76,77,77	0
7	PII	A	405	56/56	0.85	0.25	45,57,64,66	11
8	MG	A	406	1/1	0.89	0.26	62,62,62,62	0
6	NAG	A	402	14/15	0.91	0.15	51,53,55,55	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PII A 405:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.